

### AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0026] on page 8 of the specification as filed with the following:

[0026] In some embodiments, the domain corresponding to residues 1-167 of Figure 2 comprises a sequence according to Formula (I) (SEQ ID NO: 05):

Ser- $\Phi$ aa<sub>1</sub>- $\Phi$ aa<sub>2</sub>-Zaa-Xaa<sub>1</sub>- $\Phi$ aa<sub>3</sub>- $\Phi$ aa<sub>4</sub>-Xaa<sub>2</sub>-Baa<sub>1</sub>- $\Sigma$ aa<sub>1</sub>-Xaa<sub>3</sub>-Asn-Xaa<sub>4</sub>-Xaa<sub>5</sub>- $\Phi$ aa<sub>5</sub>-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Leu-Xaa<sub>8</sub>-Xaa<sub>9</sub>-Xaa<sub>10</sub>-Xaa<sub>11</sub>-Xaa<sub>12</sub>-Xaa<sub>13</sub>-Baa<sub>2</sub>-Xaa<sub>14</sub>- $\Delta$ aa<sub>1</sub>-Leu-Xaa<sub>15</sub>-Xaa<sub>16</sub>-Leu-Xaa<sub>17</sub>-Xaa<sub>18</sub>- $\Sigma$ aa<sub>2</sub>-Leu-Leu-Arg-Xaa<sub>19</sub>-His- $\Sigma$ aa<sub>3</sub>- $\Phi$ aa<sub>6</sub>-Leu- $\Delta$ aa<sub>2</sub>- $\Omega$ aa<sub>1</sub>-Ala- $\Omega$ aa<sub>2</sub>- $\Sigma$ aa<sub>4</sub>-Arg-Xaa<sub>20</sub>-Xaa<sub>21</sub>-Xaa<sub>22</sub>-Xaa<sub>23</sub>-Xaa<sub>24</sub>-Xaa<sub>25</sub>-Xaa<sub>26</sub>-Ser-Leu-Val-Xaa<sub>27</sub>- $\Phi$ aa<sub>7</sub>- $\Phi$ aa<sub>8</sub>-Xaa<sub>28</sub>-Xaa<sub>29</sub>-Leu-Lys- $\Delta$ aa<sub>3</sub>-Xaa<sub>30</sub>-Ala-Tyr-Asp-Ala- $\Delta$ aa<sub>4</sub>-Asp- $\Phi$ aa<sub>9</sub>-Leu- $\Delta$ aa<sub>5</sub>-Glu- $\Phi$ aa<sub>10</sub>-Glu-Xaa<sub>31</sub>-Xaa<sub>32</sub>-Ala-Xaa<sub>33</sub>-Baa<sub>3</sub>-Xaa<sub>34</sub>-Lys-Val (I)

wherein: each of  $\Phi$ <sub>1-10</sub> is independently selected from any hydrophobic amino acid residue, Zaa is a neutral/polar amino acid residue, each of  $\Sigma$ <sub>aa1-4</sub> is independently selected from any small amino acid residue, each of Baa<sub>3</sub> is independently selected from any basic amino acid residue, each of  $\Delta$ <sub>aa1-5</sub> is independently selected from any acidic amino acid residue, each of  $\Omega$ <sub>aa1-2</sub> is independently selected from any charged amino acid residue, and Xaa<sub>1-33</sub> are each independently selected from any amino acid residue.

Please replace paragraph [0037] on pages 10-11 of the specification as filed with the following:

[0037] In some embodiments, the domain corresponding to residues 168-536 of Figure 2 comprises a sequence according to Formula (II) (SEQ ID NO: 06):

Arg-Xaa<sub>1</sub>-Xaa<sub>2</sub>-Thr- $\Sigma$ aa<sub>1</sub>-Ser- $\Phi$ aa<sub>1</sub>-Leu-Thr-Glu- $\Sigma$ aa<sub>2</sub>-Xaa<sub>3</sub>- $\Phi$ aa<sub>2</sub>- $\Phi$ aa<sub>3</sub>-Gly-Arg-Xaa<sub>4</sub>-Gln- $\Delta$ aa<sub>1</sub>-Baa<sub>1</sub>-Glu-Xaa<sub>5</sub>- $\Phi$ aa<sub>4</sub>- $\Phi$ aa<sub>5</sub>- $\Omega$ aa<sub>1</sub>-Leu-Leu-Leu- $\Delta$ aa<sub>2</sub>- $\Sigma$ aa<sub>3</sub>- $\Sigma$ aa<sub>4</sub>-Xaa<sub>6</sub>-Gly-Xaa<sub>7</sub>-Xaa<sub>8</sub>- $\Sigma$ aa<sub>5</sub>-Phe- $\Sigma$ aa<sub>6</sub>-Val- $\Phi$ aa<sub>6</sub>-Pro- $\Phi$ aa<sub>7</sub>-Val-Gly- $\Phi$ aa<sub>8</sub>-Gly-Gly-Xaa<sub>9</sub>-Gly-Lys-Thr-Thr-Leu- $\Sigma$ aa<sub>7</sub>-Gln-Leu- $\Phi$ aa<sub>9</sub>- $\Phi$ aa<sub>10</sub>-Asn-Asp-Xaa<sub>10</sub>-Arg-Val-Xaa<sub>11</sub>-Xaa<sub>12</sub>-Xaa<sub>13</sub>-Phe-Xaa<sub>14</sub>-Leu-Baa<sub>2</sub>- $\Phi$ aa<sub>11</sub>-Trp-Val-Cys-Val-Ser-Asp-Xaa<sub>15</sub>-Phe-Xaa<sub>16</sub>-Val-Lys-Arg- $\Phi$ aa<sub>12</sub>-Thr-Baa<sub>3</sub>-Glu-Ile-Xaa<sub>17</sub>-Glu-Xaa<sub>18</sub>-Ala-Thr-Xaa<sub>19</sub>-Xaa<sub>20</sub>- $\Omega$ aa<sub>2</sub>-Xaa<sub>21</sub>-Xaa<sub>22</sub>-Asp-Xaa<sub>23</sub>-Xaa<sub>24</sub>-Asn-Leu-Xaa<sub>25</sub>-Xaa<sub>26</sub>-Leu-Gln-Xaa<sub>27</sub>-Xaa<sub>28</sub>-Leu-Lys-Glu- $\Omega$ aa<sub>3</sub>-Ile-Xaa<sub>29</sub>- $\Sigma$ aa<sub>8</sub>-Xaa<sub>30</sub>-Xaa<sub>31</sub>-Phe-Leu-Leu-Val-Leu-Asp-Asp-Val-Trp

Xaa<sub>32</sub>-Glu-Xaa<sub>33</sub>-Xaa<sub>34</sub>-Xaa<sub>35</sub>-Ωaa<sub>4</sub>-Trp-Glu-Xaa<sub>36</sub>-Leu-Xaa<sub>37</sub>-Ala-Pro-Leu-Ωaa<sub>5</sub>-Xaa<sub>38</sub>-Σaa<sub>9</sub>-  
Σaa<sub>10</sub>-Arg-Gly-Ser-Xaa<sub>39</sub>-Val-Ile-Val-Thr-Thr-Xaa<sub>40</sub>-Xaa<sub>41</sub>-Xaa<sub>42</sub>-Lys-Φaa<sub>13</sub>-Ala-Xaa<sub>43</sub>- Φaa<sub>14</sub>-  
Xaa<sub>44</sub>-Gly-Thr-Met-Ωaa<sub>6</sub>-Xaa<sub>45</sub>-Φaa<sub>15</sub>-Xaa<sub>46</sub>-Leu-Åaa<sub>3</sub>-Xaa<sub>47</sub>-Leu-Xaa<sub>48</sub>-Åaa<sub>4</sub>-Asp-Xaa<sub>49</sub>-Xaa<sub>50</sub>-  
Trp-Xaa<sub>51</sub>-Leu-Φaa<sub>16</sub>-Ωaa<sub>7</sub>-Xaa<sub>52</sub>-Xaa<sub>53</sub>-Σaa<sub>11</sub>-Phe-Xaa<sub>54</sub>-Xaa<sub>55</sub>-Xaa<sub>56</sub>-Xaa<sub>57</sub>-Xaa<sub>58</sub>-Σaa<sub>12</sub>-Xaa<sub>59</sub>-  
Xaa<sub>60</sub>-Xaa<sub>61</sub>-Xaa<sub>62</sub>-Ωaa<sub>8</sub>-Φaa<sub>17</sub>-Glu-Xaa<sub>63</sub>-Ile-Gly-Arg-Lys-Ile-Ala-Xaa<sub>64</sub>-Lys-Φaa<sub>18</sub>-Xaa<sub>65</sub>-Gly-  
Xaa<sub>66</sub>-Pro-Φaa<sub>19</sub>-Σaa<sub>13</sub>-Ala-Xaa<sub>67</sub>-Σaa<sub>14</sub>-Φaa<sub>20</sub>-Gly-Xaa<sub>68</sub>-Φaa<sub>21</sub>-Leu-Arg-Xaa<sub>69</sub>-Ωaa<sub>9</sub>-Xaa<sub>70</sub>-  
Σaa<sub>15</sub>-Xaa<sub>71</sub>-Xaa<sub>72</sub>-Xaa<sub>73</sub>-Trp-Arg-Xaa<sub>74</sub>-Φaa<sub>22</sub>-Φaa<sub>23</sub>-Glu-Σaa<sub>16</sub>-Glu-Xaa<sub>75</sub>-Trp-Xaa<sub>76</sub>-Φaa<sub>24</sub>-  
Pro-Xaa<sub>77</sub>-Ala-Xaa<sub>78</sub>-Xaa<sub>79</sub>-Åaa<sub>5</sub>-Φaa<sub>25</sub>-Leu-Σaa<sub>17</sub>-Xaa<sub>80</sub>-Leu-Xaa<sub>81</sub>-Xaa<sub>82</sub>-Ser-Tyr-Xaa<sub>83</sub>-Xaa<sub>84</sub>-  
Leu-Pro-Σaa<sub>18</sub>-Xaa<sub>85</sub>-Leu-Baa<sub>4</sub>-Xaa<sub>86</sub>-Cys-Phe-Ala-Phe-Cys-Ala-Φaa<sub>26</sub>-Phe-Xaa<sub>87</sub>-Lys-Xaa<sub>88</sub>-  
'Tyr-Xaa<sub>89</sub>-Phe-Xaa<sub>90</sub>-Lys-Ωaa<sub>10</sub>-Xaa<sub>91</sub>-Leu-Ile-Xaa<sub>92</sub>-Xaa<sub>93</sub>-Trp-Ile-Ala-Xaa<sub>94</sub>-Xaa<sub>95</sub>-Φaa<sub>27</sub>-Ile  
(II)

wherein: each of Φ<sub>1-27</sub> is independently selected from any hydrophobic amino acid residue,  
each of Σaa<sub>1-18</sub> is independently selected from any small amino acid residue,  
each of Baa<sub>1-4</sub> is independently selected from any basic amino acid residue,  
each of Åaa<sub>1-5</sub> is independently selected from any acidic amino acid residue,  
each of Ωaa<sub>1-10</sub> is independently selected from any charged amino acid residue,  
and  
Xaa<sub>1-95</sub> are each independently selected from any amino acid residue.

Please replace paragraph [0056] on pages 15-16 of the specification as filed with the following:

[0056] In some embodiments, the domain corresponding to residues 537-1476 of Figure 2 comprises a sequence according to Formula (III) (SEQ ID NO: 07):

Leu-Xaa<sub>1</sub>-Ωaa<sub>1</sub>-Xaa<sub>2</sub>-Φaa<sub>1</sub>-Phe-Baa<sub>1</sub>-Xaa<sub>3</sub>-Leu-Xaa<sub>4</sub>-Arg-Ile-Baa<sub>2</sub>-Val-Leu-Xaa<sub>5</sub>-Φaa<sub>2</sub>-  
Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Xaa<sub>8</sub>-Φaa<sub>3</sub>-Baa<sub>3</sub>-Xaa<sub>9</sub>-Leu-Pro-Xaa<sub>10</sub>-Xaa<sub>11</sub>- Φaa<sub>4</sub>-Gly-Xaa<sub>12</sub>-Leu-Xaa<sub>13</sub>-Xaa<sub>14</sub>-  
Leu-Arg-Tyr-Leu-Xaa<sub>15</sub>-Φaa<sub>5</sub>-Ser-Xaa<sub>16</sub>-Asn-Σaa<sub>1</sub>-Xaa<sub>17</sub>-Ile-Gln-Arg-Leu-Pro-Glu-Ser-Φaa<sub>6</sub>-  
Xaa<sub>18</sub>-Ωaa<sub>2</sub>-Leu-Xaa<sub>19</sub>-Xaa<sub>20</sub>-Leu-Gln-Σaa<sub>2</sub>-Leu-Xaa<sub>21</sub>-Leu-Xaa<sub>22</sub>-Gly-Cys-Xaa<sub>23</sub>-Leu-Xaa<sub>24</sub>-  
Xaa<sub>25</sub>-Φaa<sub>7</sub>-Pro-Xaa<sub>26</sub>-Σaa<sub>3</sub>-Met-Ser-Baa<sub>4</sub>-Leu-Φaa<sub>8</sub>-Xaa<sub>27</sub>-Leu-Arg-Gln-Leu-Baa<sub>5</sub>-Xaa<sub>28</sub>-Xaa<sub>29</sub>-  
Xaa<sub>30</sub>-Åaa<sub>1</sub>-Φaa<sub>9</sub>-Ile-Σaa<sub>4</sub>-Ωaa<sub>3</sub>-Ile-Xaa<sub>31</sub>-Ωaa<sub>4</sub>-Val-Gly-Baa<sub>6</sub>-Leu-Ile-Xaa<sub>32</sub>-Leu-Gln-Glu-Leu-  
Xaa<sub>33</sub>-Ala-Φaa<sub>10</sub>-Xaa<sub>34</sub>-Val-Xaa<sub>35</sub>-Xaa<sub>36</sub>-Baa<sub>7</sub>-Xaa<sub>37</sub>-Gly-Xaa<sub>38</sub>-Xaa<sub>39</sub>-Φaa<sub>11</sub>-Ala-Glu-Leu-Ser-

$\Sigma aa_5$ - $\Phi aa_{12}$ - $Xaa_{40}$ -Gln-Leu-Baa $_8$ - $\Sigma aa_6$ - $Xaa_{41}$ -Leu- $Xaa_{42}$ -Ile- $Xaa_{43}$ -Asn-Leu- $Xaa_{44}$ -Asn-Val-  
 $Xaa_{45}$ - $Xaa_{46}$ - $Xaa_{47}$ - $\Omega aa_5$ -Glu- $\Sigma aa_7$ - $Xaa_{48}$ -Lys-Ala-Baa $_9$ -Leu- $\Omega aa_6$ - $\Omega aa_7$ -Lys-Gln- $Xaa_{49}$ -Leu-  
 $\Omega aa_8$ - $Xaa_{50}$ -Leu- $\dot{A} aa_2$ -Leu- $\Omega aa_9$ -Trp-Ala- $Xaa_{51}$ -Gly- $Xaa_{52}$ - $Xaa_{53}$ - $Xaa_{54}$ - $Xaa_{55}$ - $Xaa_{56}$ - $Xaa_{57}$ -  
 $Xaa_{58}$ -Glu- $Xaa_{59}$ - $Xaa_{60}$ - $Xaa_{61}$ - $Xaa_{62}$ - $\Omega aa_{10}$ - $\Omega aa_{11}$ -Val-Leu- $Xaa_{63}$ -Gly-Leu- $Xaa_{64}$ -Pro-His- $Xaa_{65}$ -  
 $Xaa_{66}$ -Leu-Baa $_{10}$ - $Xaa_{67}$ -Leu- $\Sigma aa_8$ -Ile-Baa $_{11}$ - $Xaa_{68}$ -Tyr- $\Sigma aa_9$ -Gly- $\Sigma aa_{10}$ - $\Sigma aa_{11}$ - $Xaa_{69}$ -Pro-Ser-Trp-  
 $\Phi aa_{13}$ - $Xaa_{70}$ - $Xaa_{71}$ - $Xaa_{72}$ - $\Phi aa_{14}$ -Leu-Pro-Asn- $\Phi aa_{15}$ - $Xaa_{73}$ -Thr- $\Phi aa_{16}$ -Baa $_{12}$ -Leu- $\Omega aa_{12}$ - $Xaa_{74}$ -  
Cys- $\Sigma aa_{12}$ -Arg-Leu- $Xaa_{75}$ - $Xaa_{76}$ -Leu- $\Sigma aa_{13}$ - $Xaa_{77}$ - $\Phi aa_{17}$ -Gly-Gln-Leu- $Xaa_{78}$ - $Xaa_{79}$ -Leu-Baa $_{13}$ -  
 $Xaa_{80}$ -Leu-His- $\Phi aa_{18}$ - $\Omega aa_{13}$ - $Xaa_{81}$ -Met- $\Sigma aa_{14}$ - $Xaa_{82}$ -Val-Baa $_{14}$ -Gln- $\Phi aa_{19}$ - $Xaa_{83}$ - $Xaa_{84}$ - $Xaa_{85}$ -  
 $\Phi aa_{20}$ - $Xaa_{86}$ -Gly- $Xaa_{87}$ - $\Sigma aa_{15}$ - $\Omega aa_{14}$ - $Xaa_{88}$ - $Xaa_{89}$ - $Xaa_{90}$ -Phe-Pro- $Xaa_{91}$ -Leu-Glu- $Xaa_{92}$ -Leu-  
 $Xaa_{93}$ - $\Phi aa_{21}$ - $\Omega aa_{15}$ - $\Omega aa_{16}$ -Met-Pro- $\Sigma aa_{16}$ -Leu- $\Omega aa_{17}$ -Glu- $\Phi aa_{22}$  (III)

wherein: each of  $\Phi_{1-22}$  is independently selected from any hydrophobic amino acid residue,  
each of  $\Sigma aa_{1-6}$  is independently selected from any small amino acid residue,  
each of Baa $_{1-14}$  is independently selected from any basic amino acid residue,  
each of  $\dot{A} aa_{1-2}$  is independently selected from any acidic amino acid residue,  
each of  $\Omega aa_{1-16}$  is independently selected from any charged amino acid residue,  
and  
 $Xaa_{1-93}$  are each independently selected from any amino acid residue.